

FIG. 1

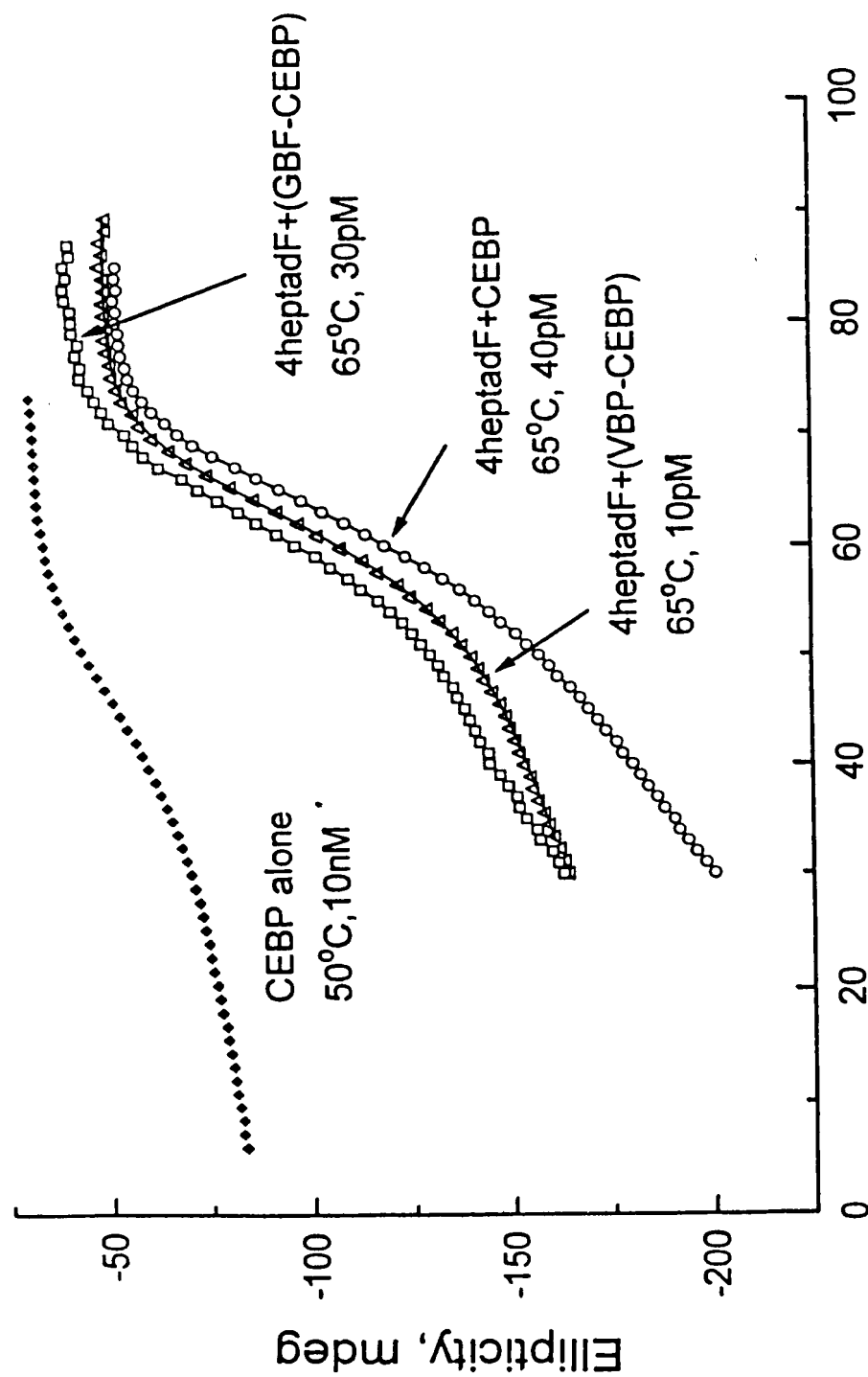


FIG. 2

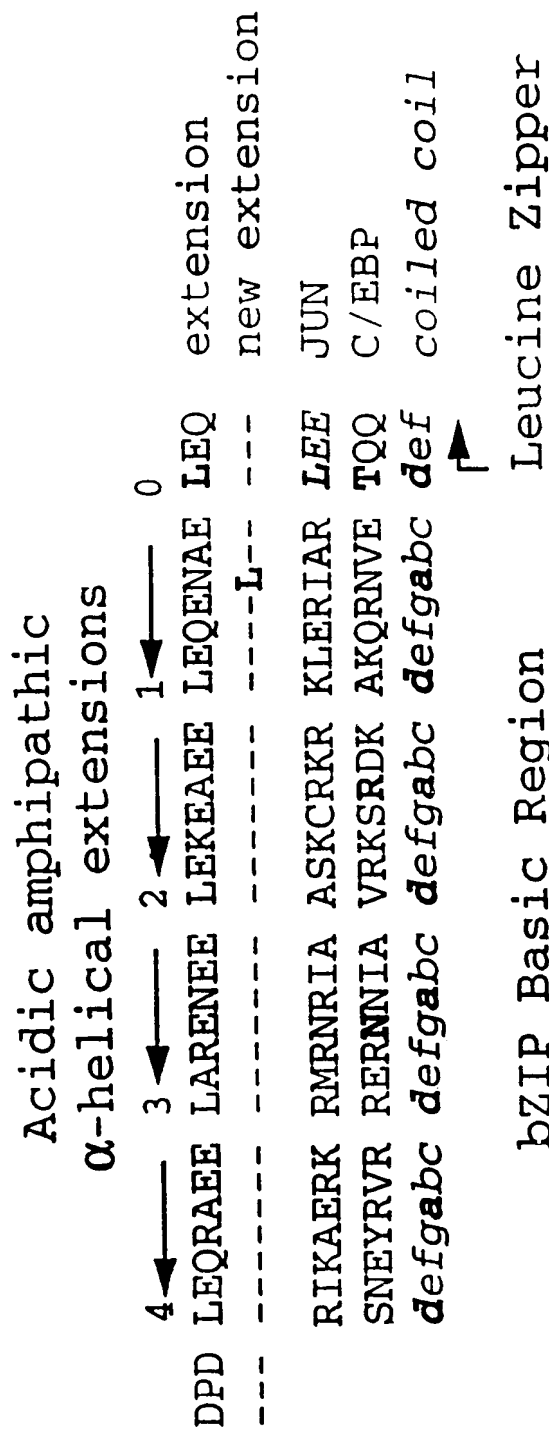


FIG. 3

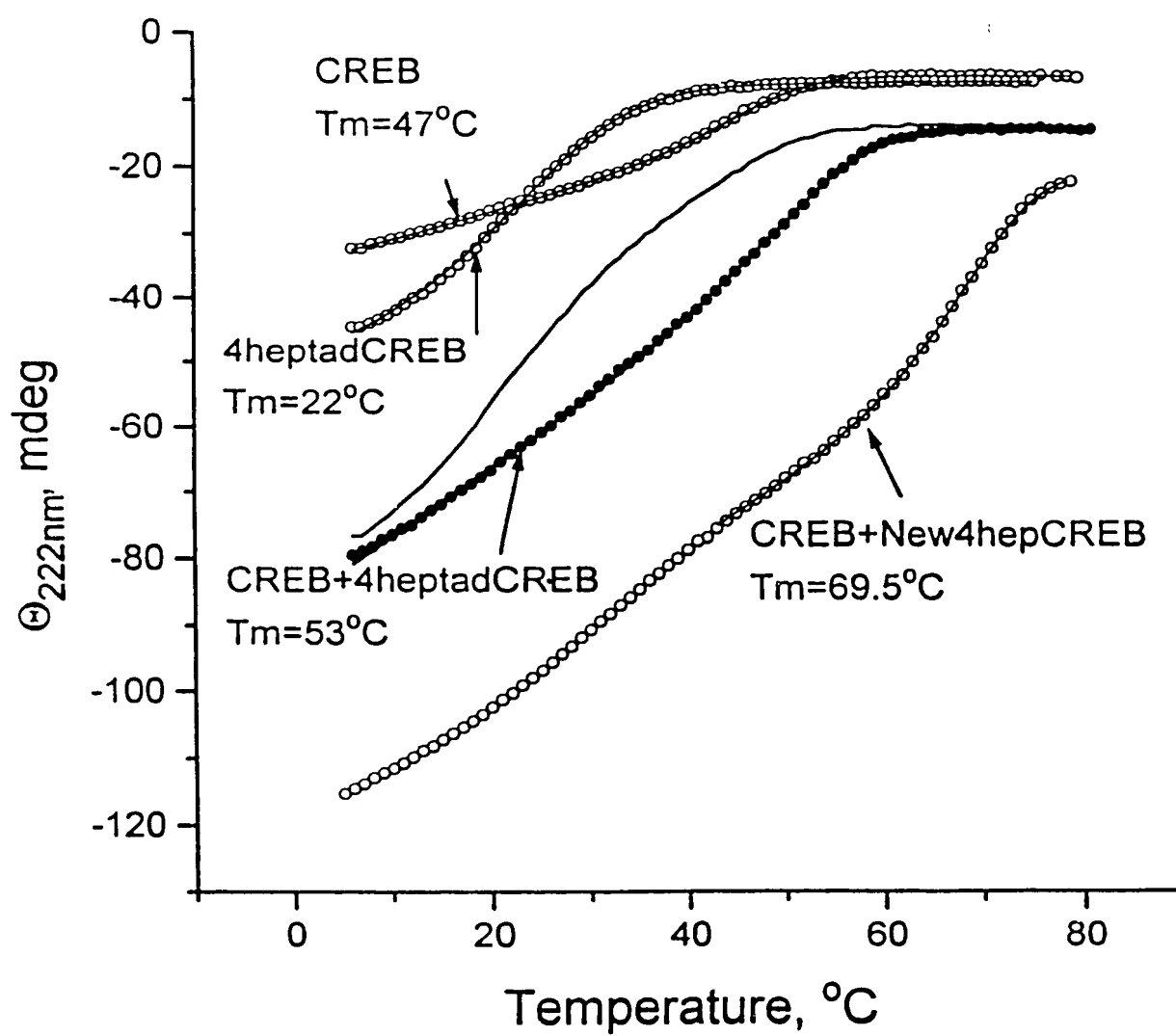


FIG. 4

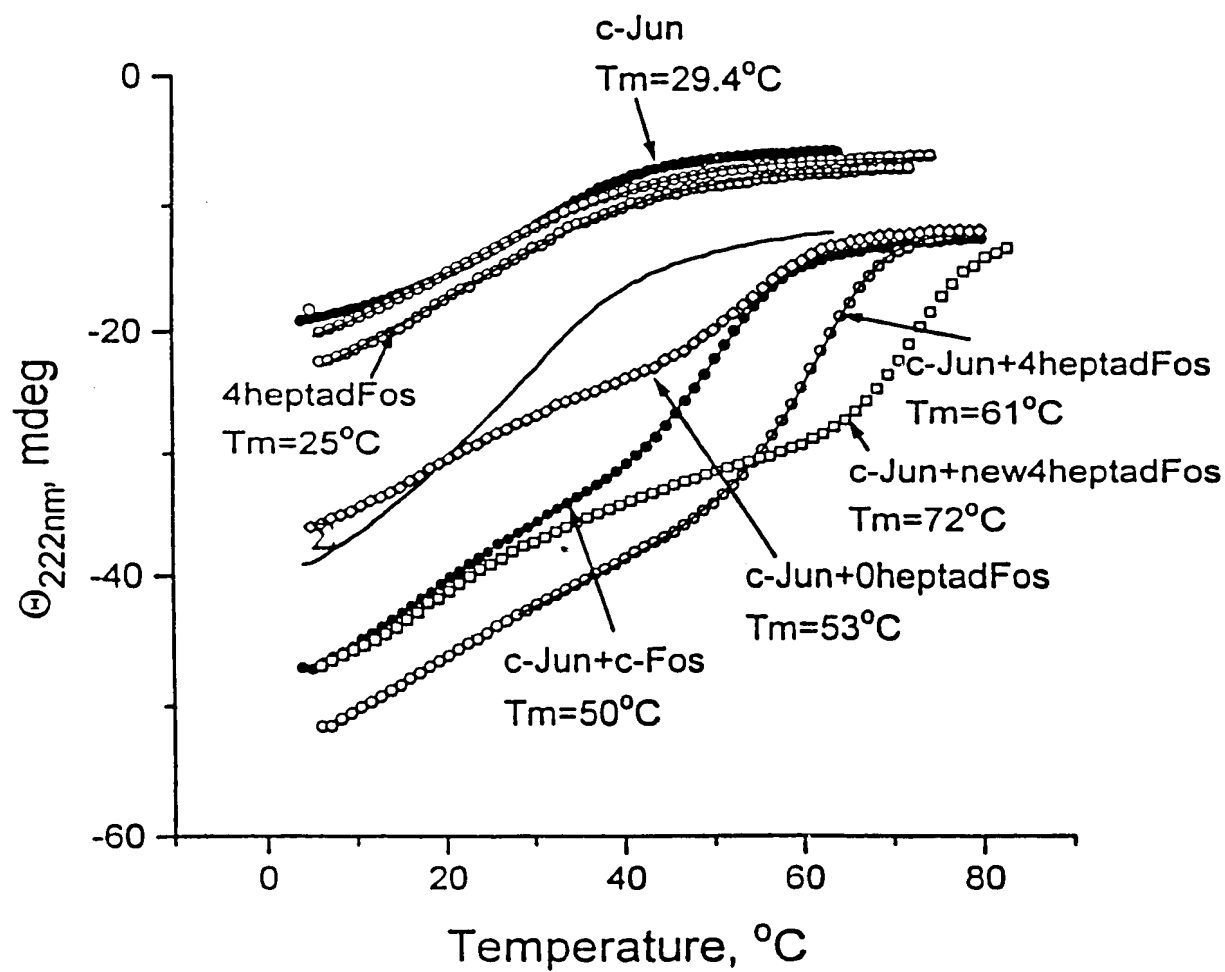


FIG. 5A

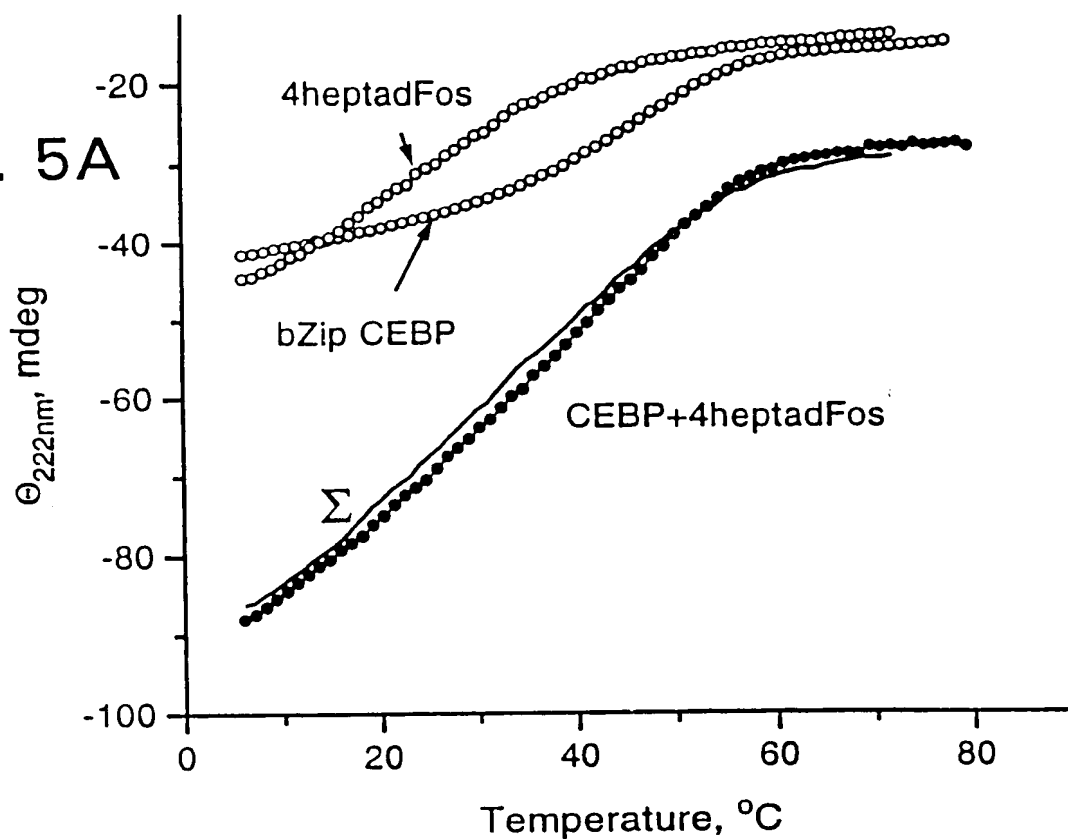


FIG. 5B

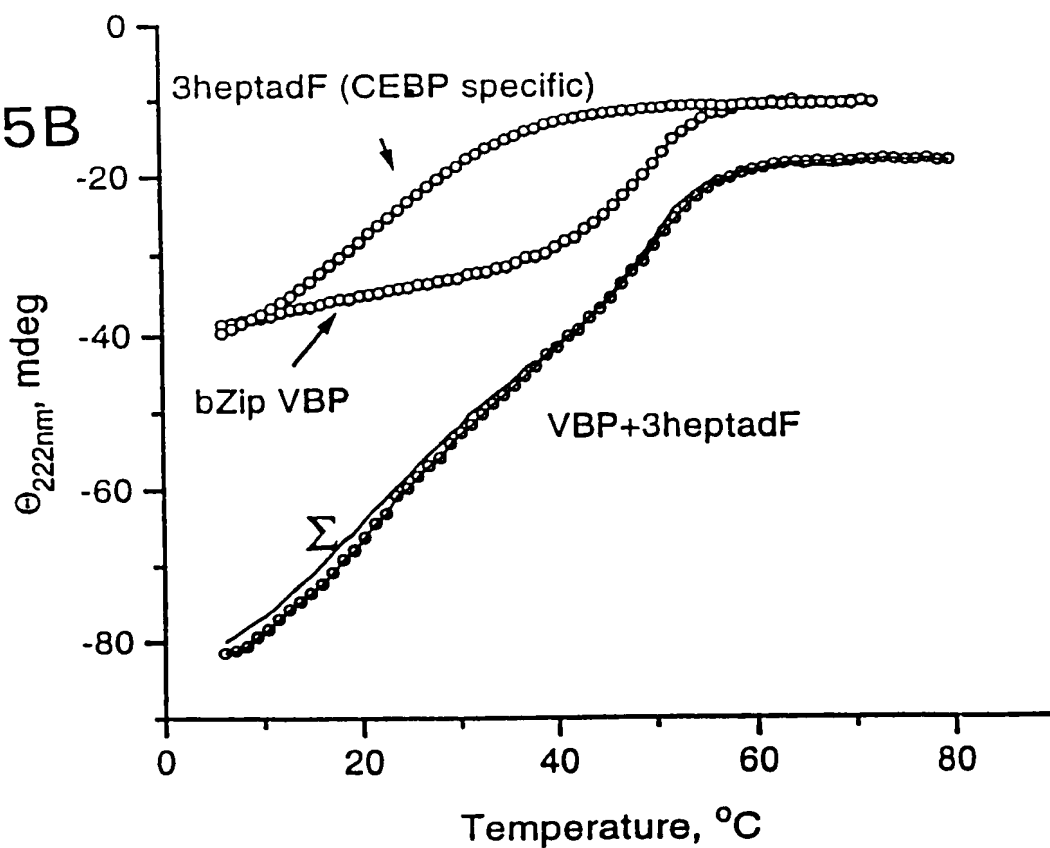


FIG. 6

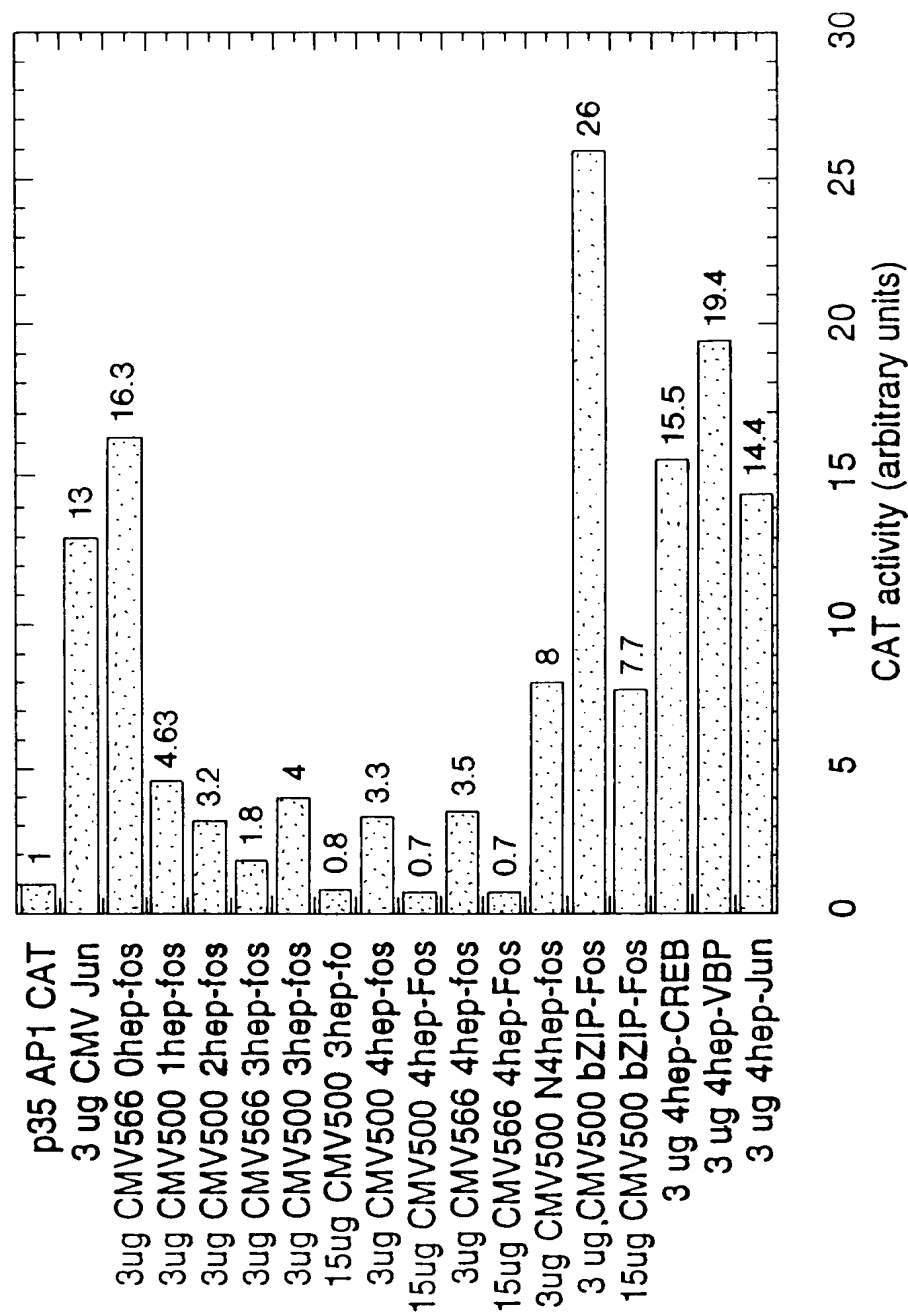
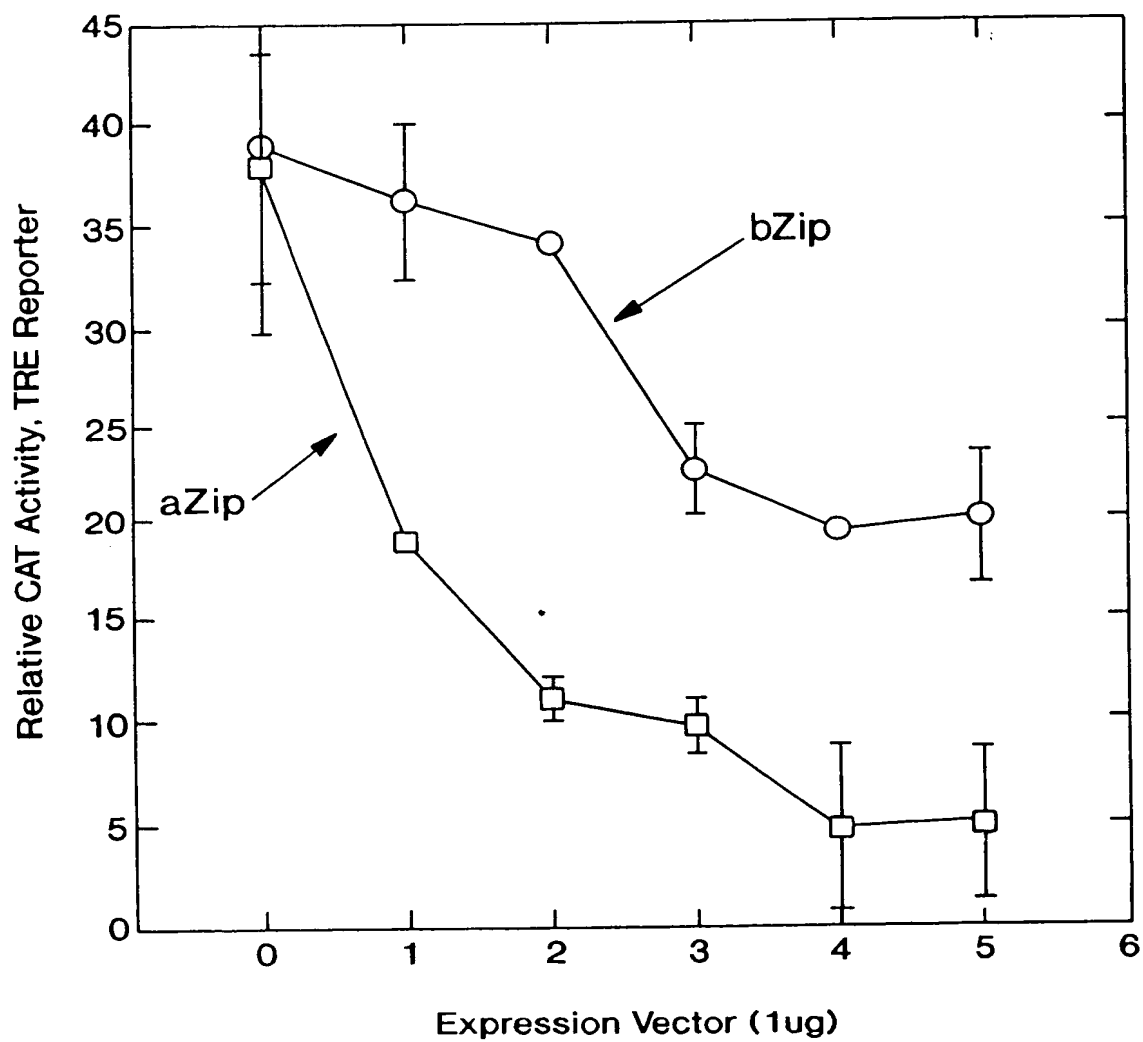


FIG. 7



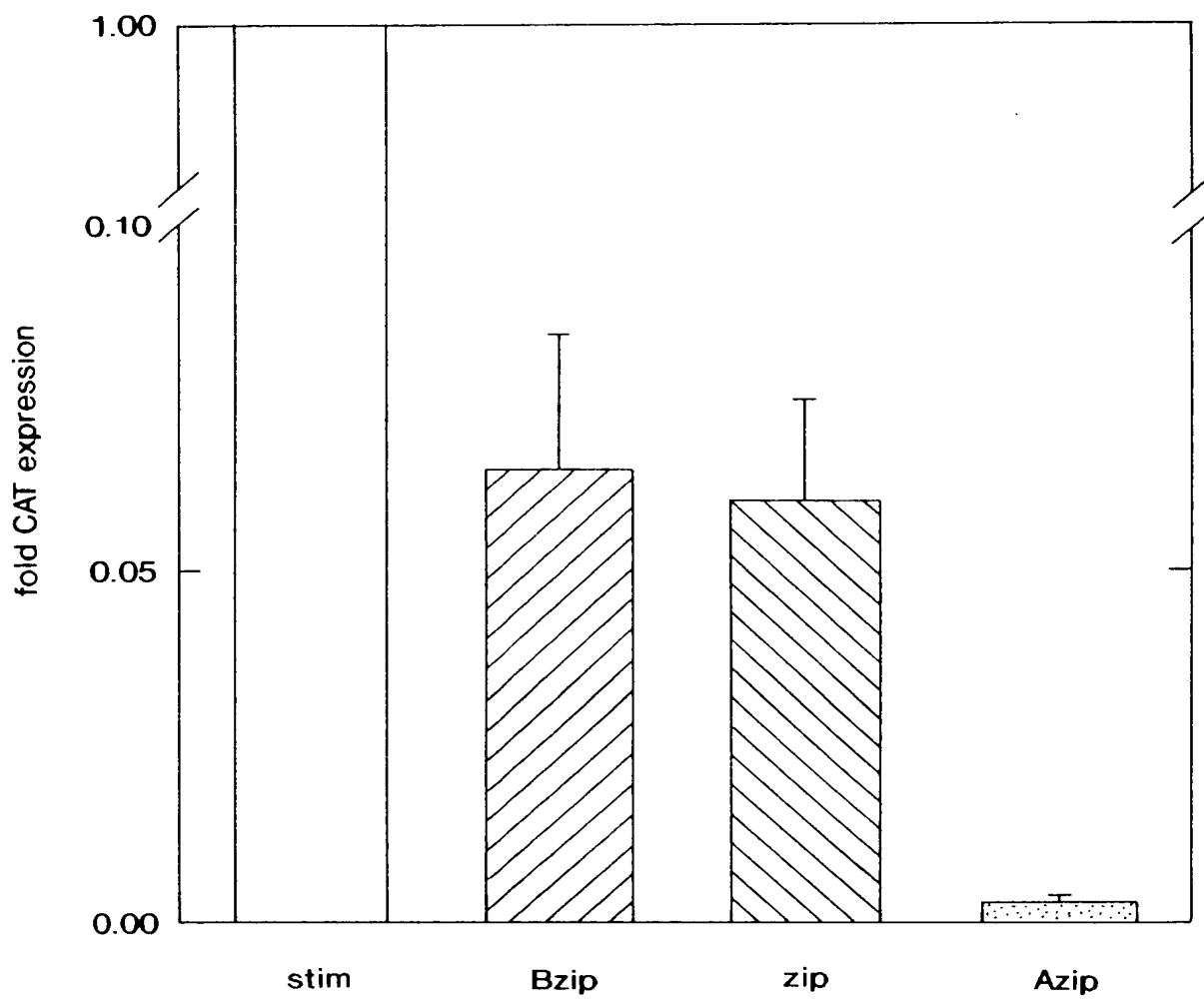


FIG. 8

FIG. 9

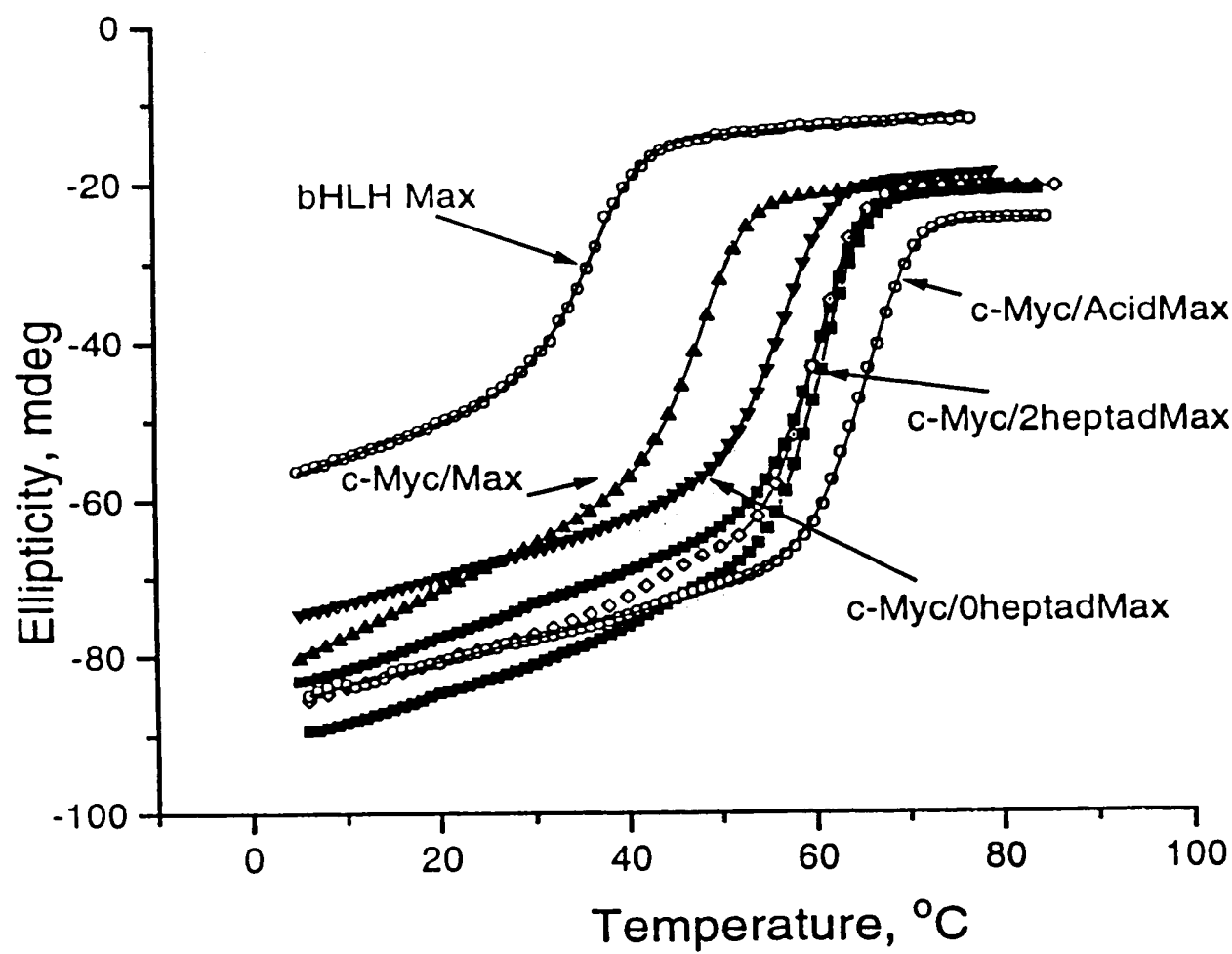


FIG. 10A

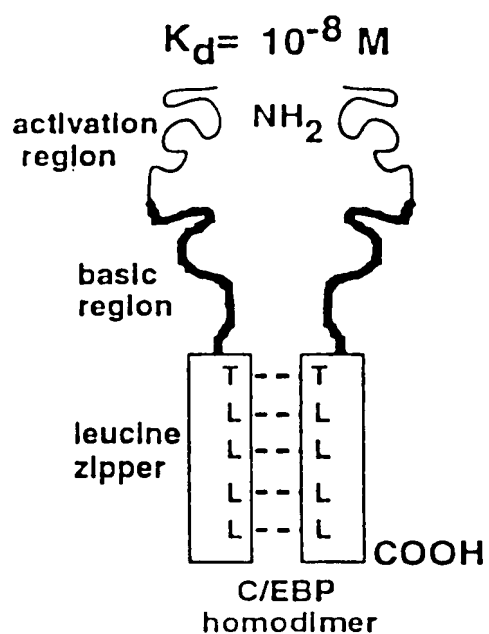
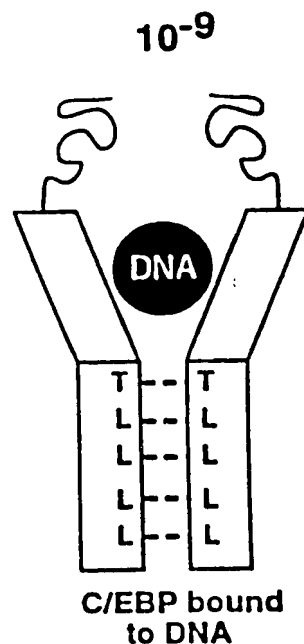


FIG. 10B



7×10^{-9}

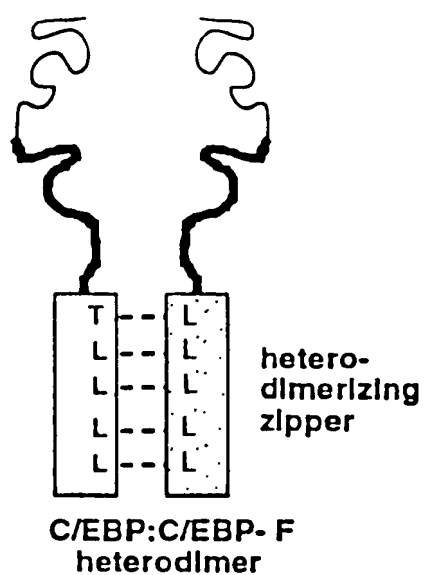


FIG. 10C

3×10^{-9}

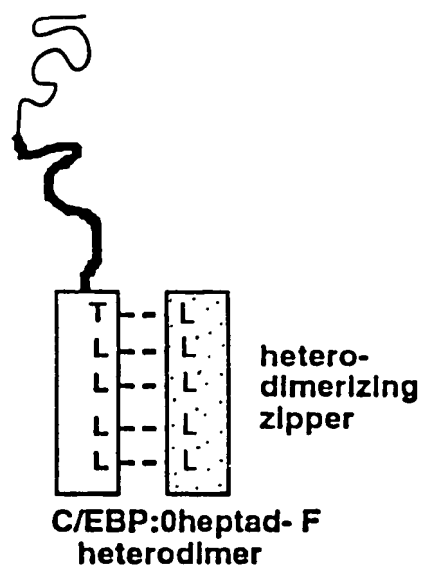


FIG. 10D

FIG. 11A

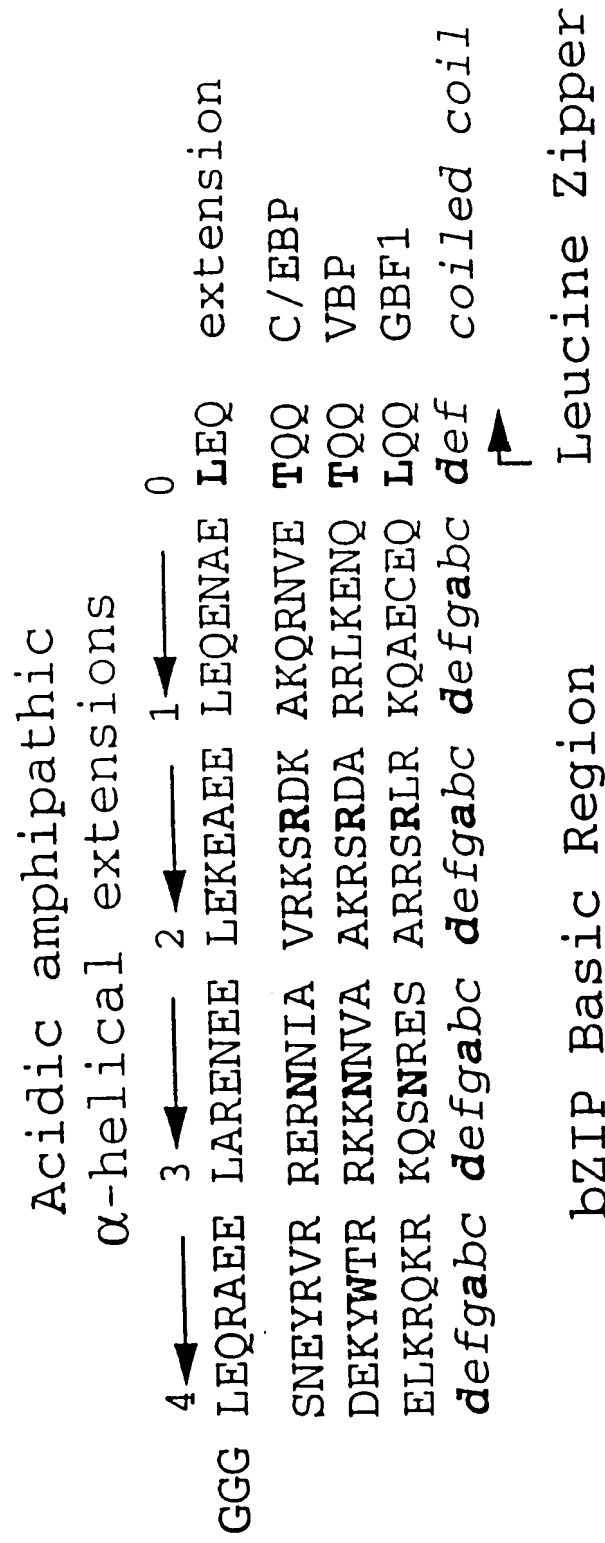


FIG. 11B

bZIP Basic Region

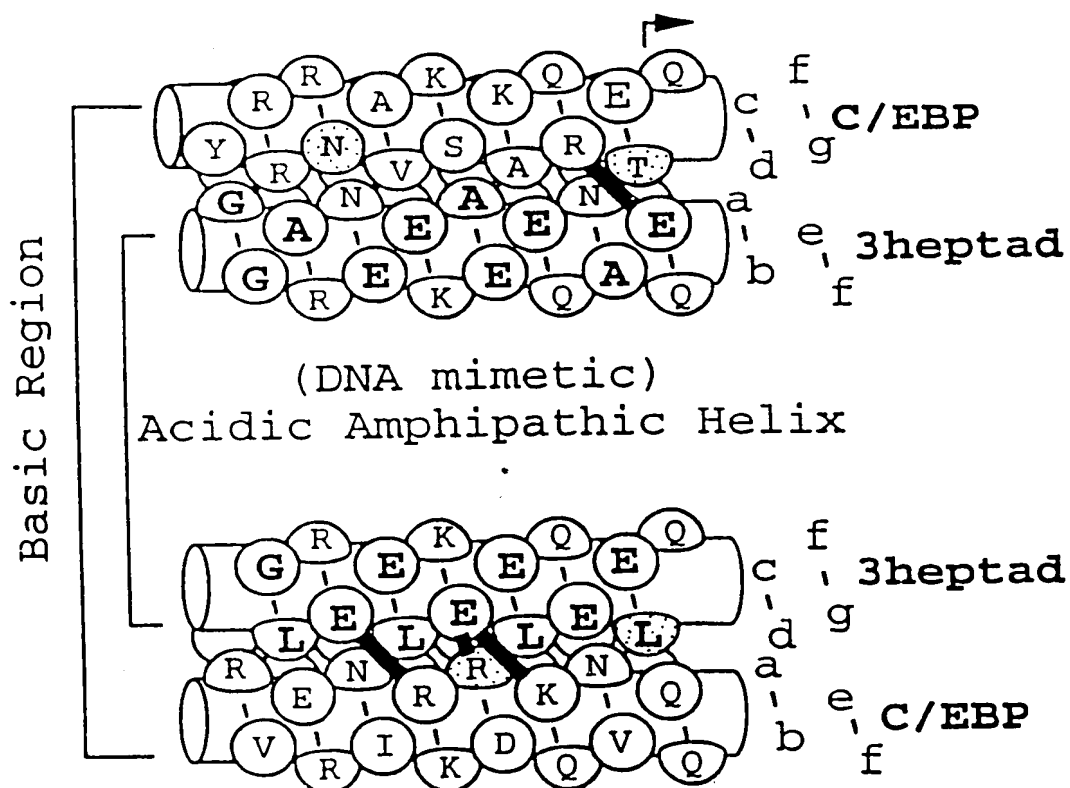


FIG. 11C

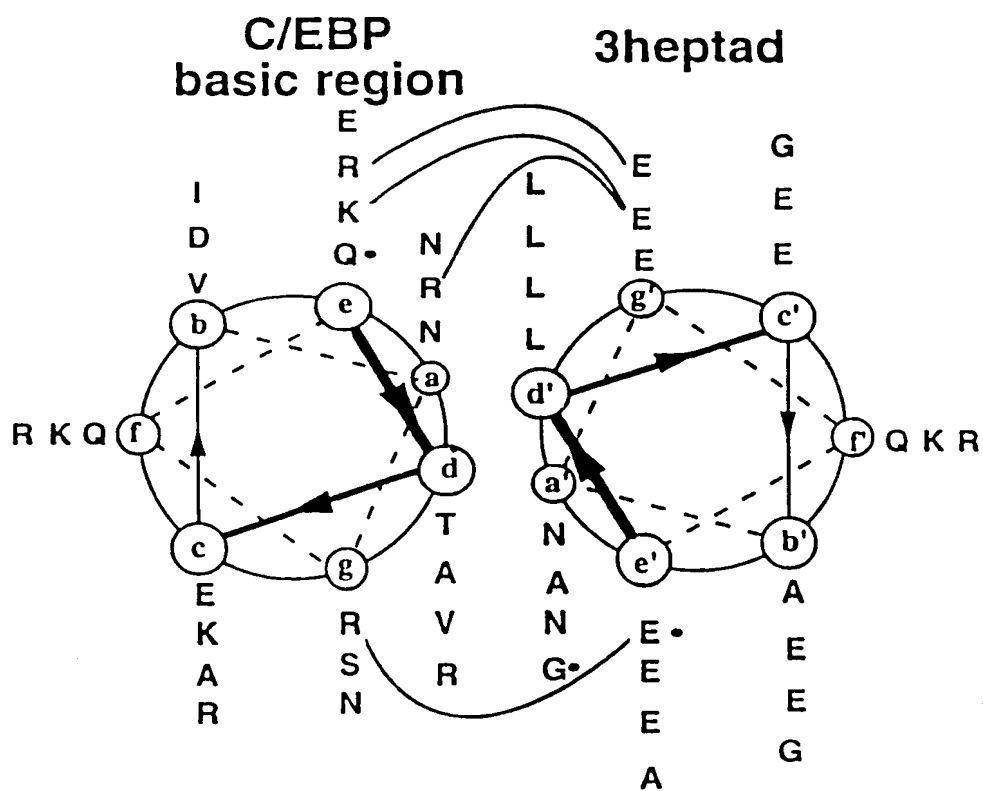


FIG. 12

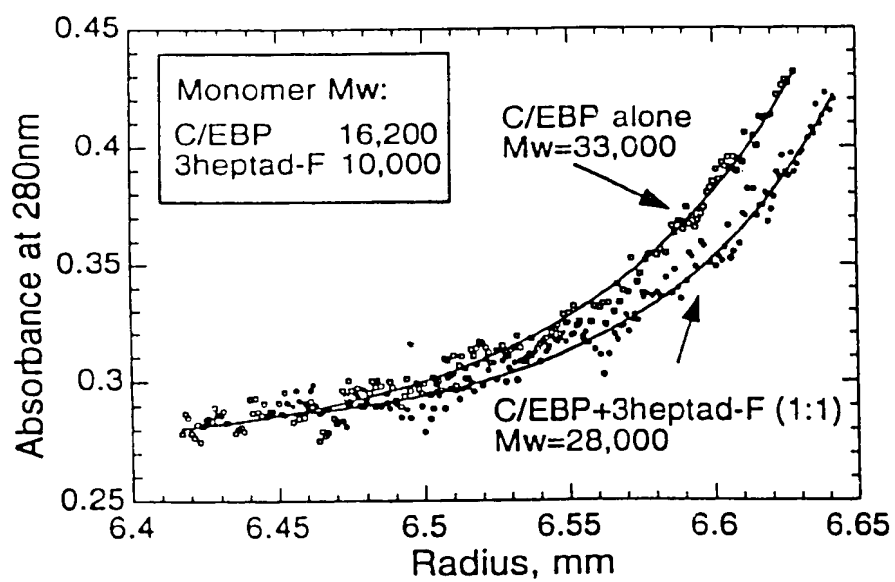


FIG. 13A

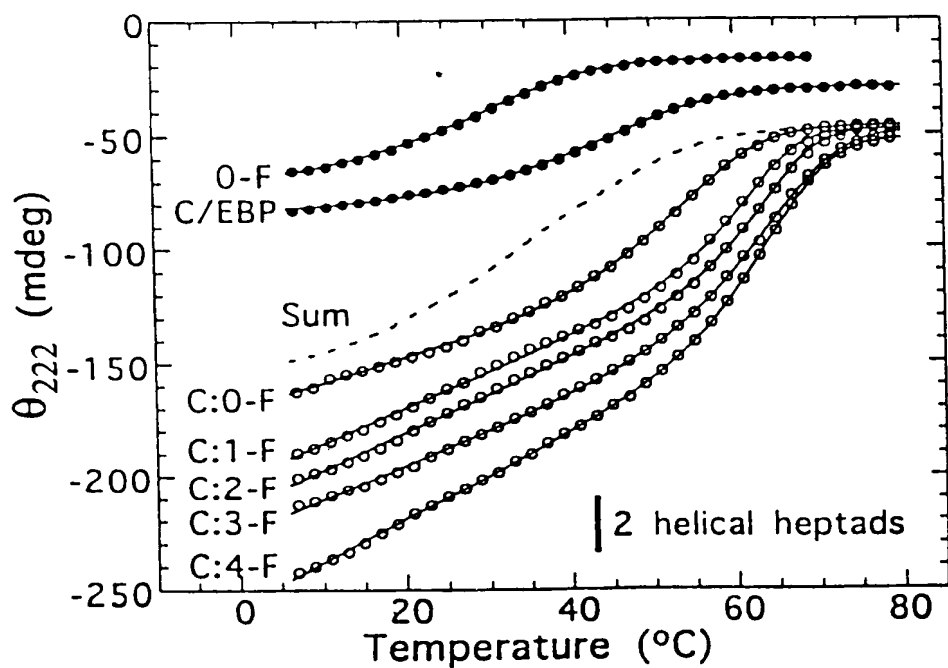
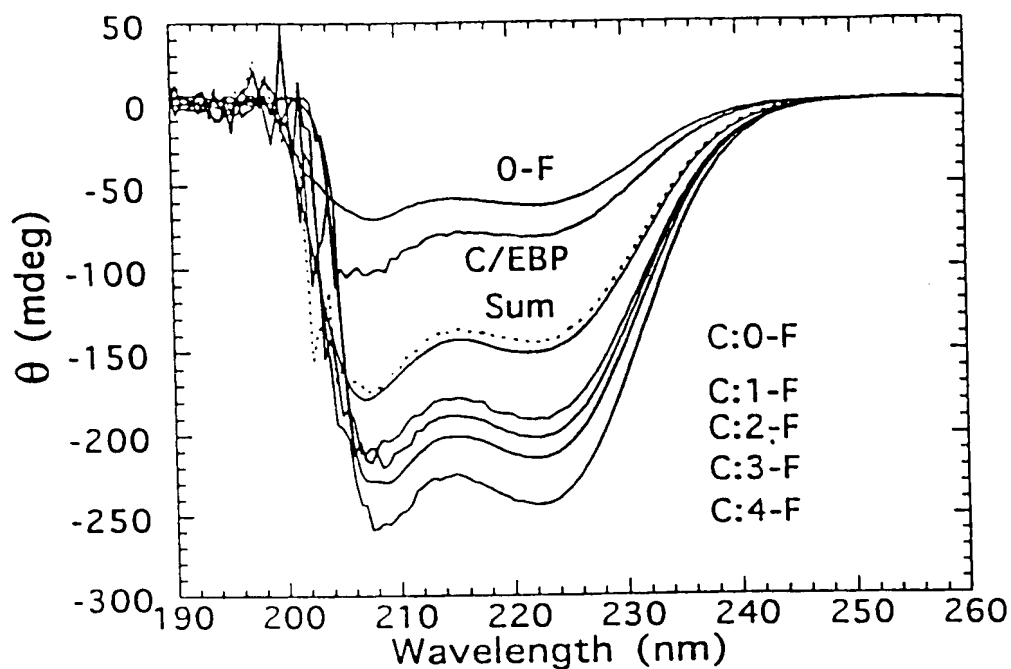


FIG. 13B

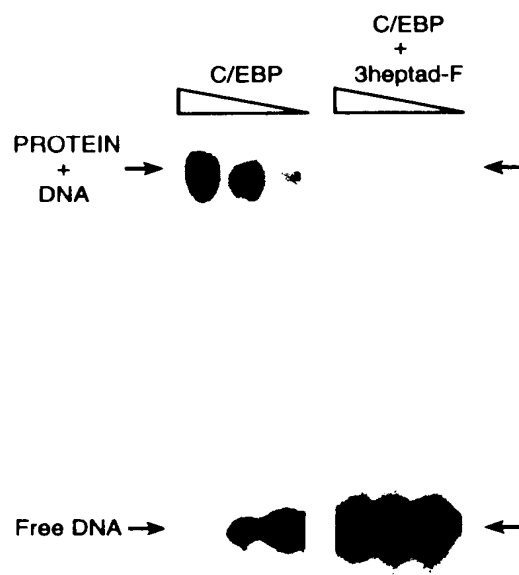


FIG. 14A

FIG. 14B

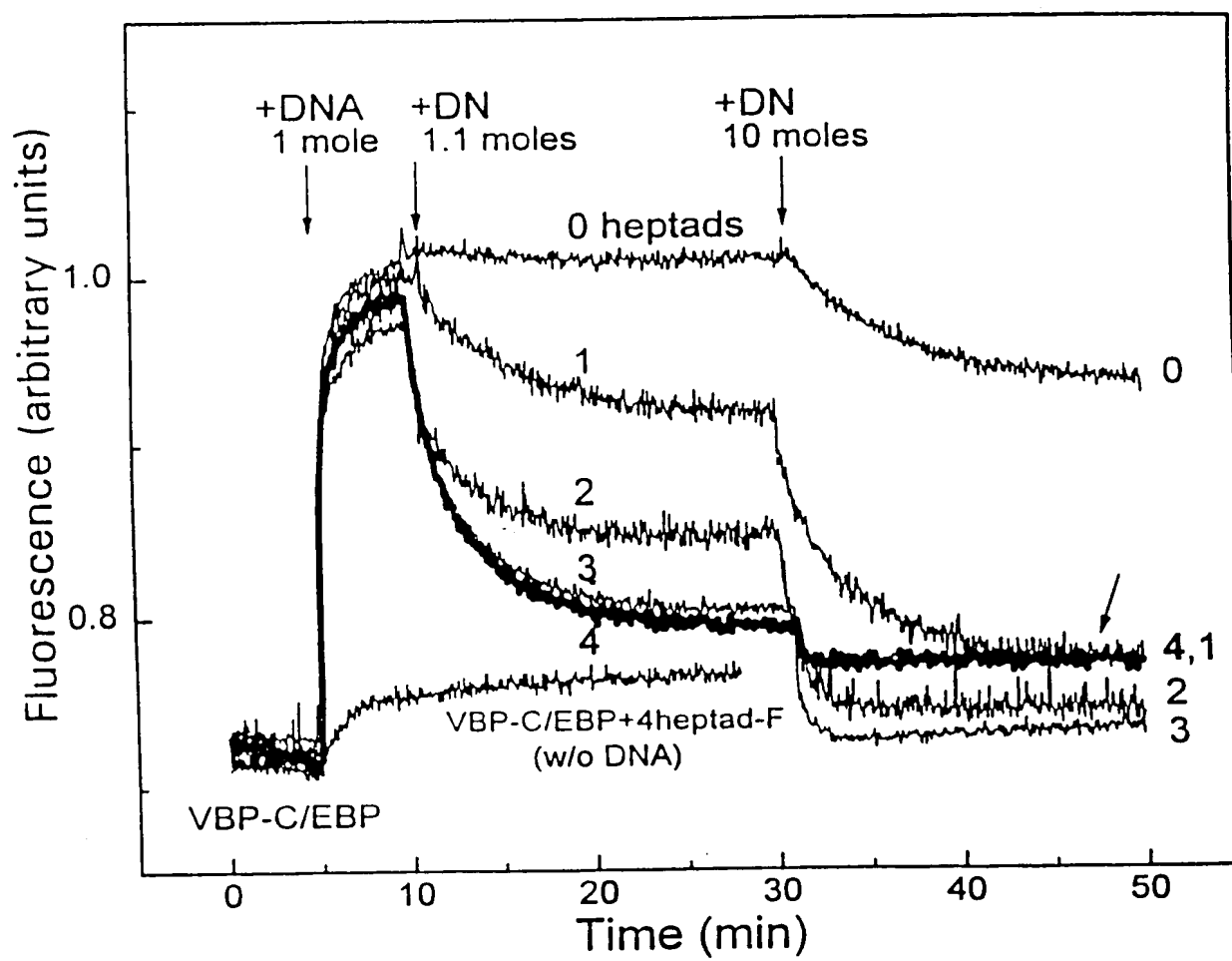


FIG. 15

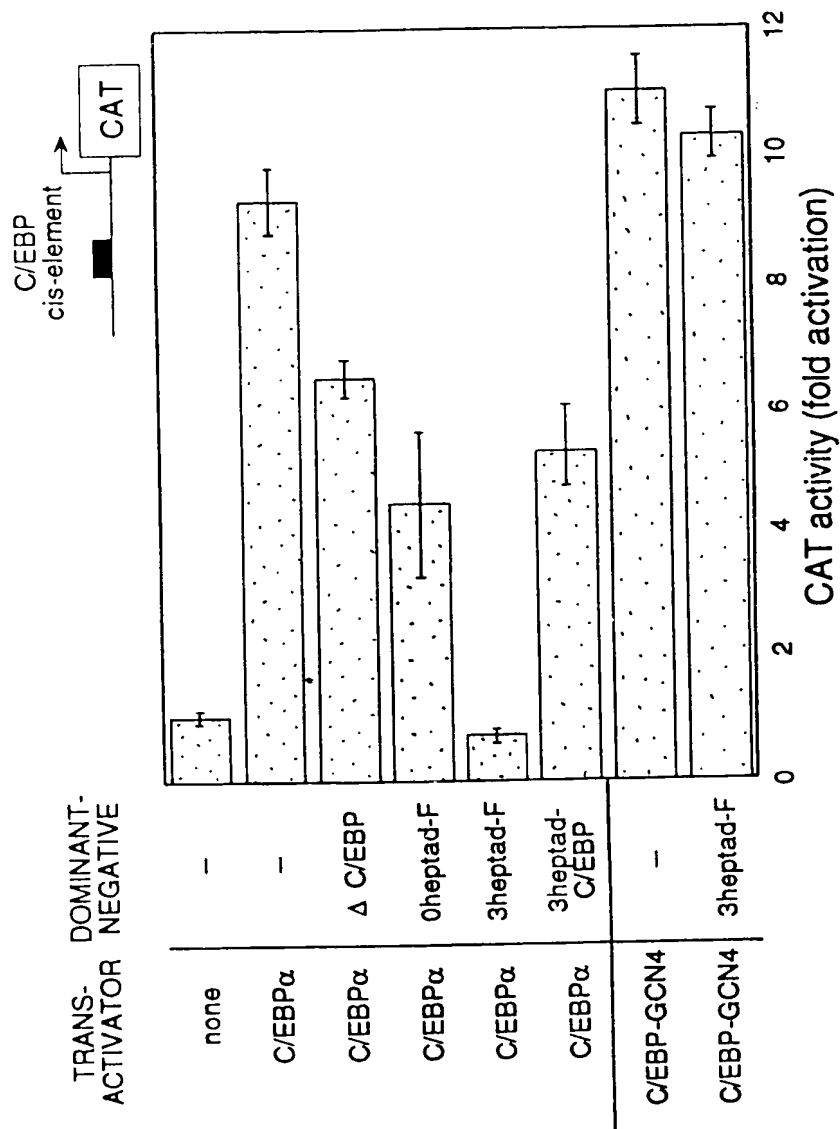


FIG. 16A

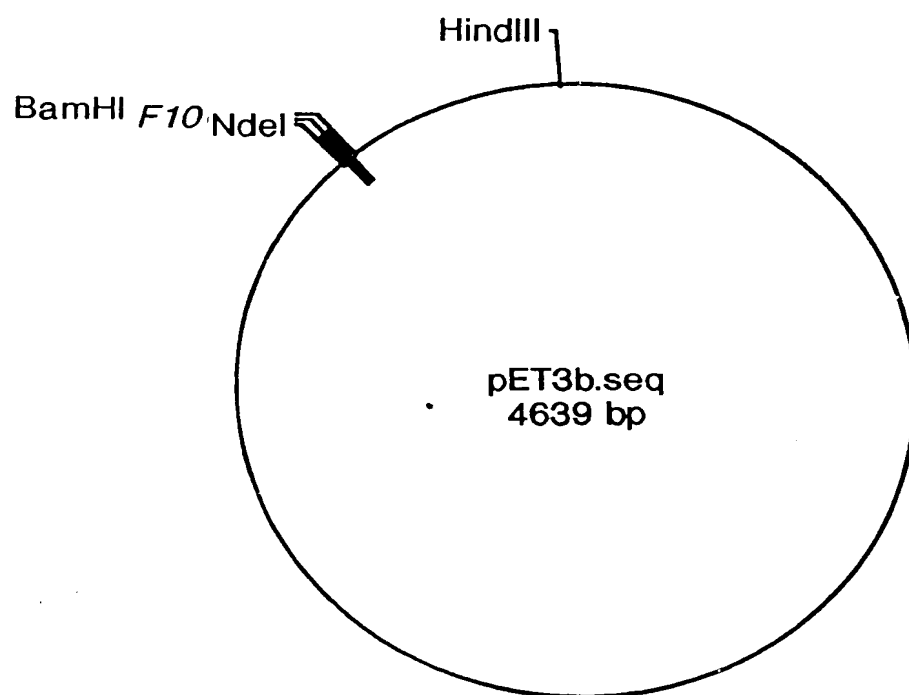


FIG. 16B

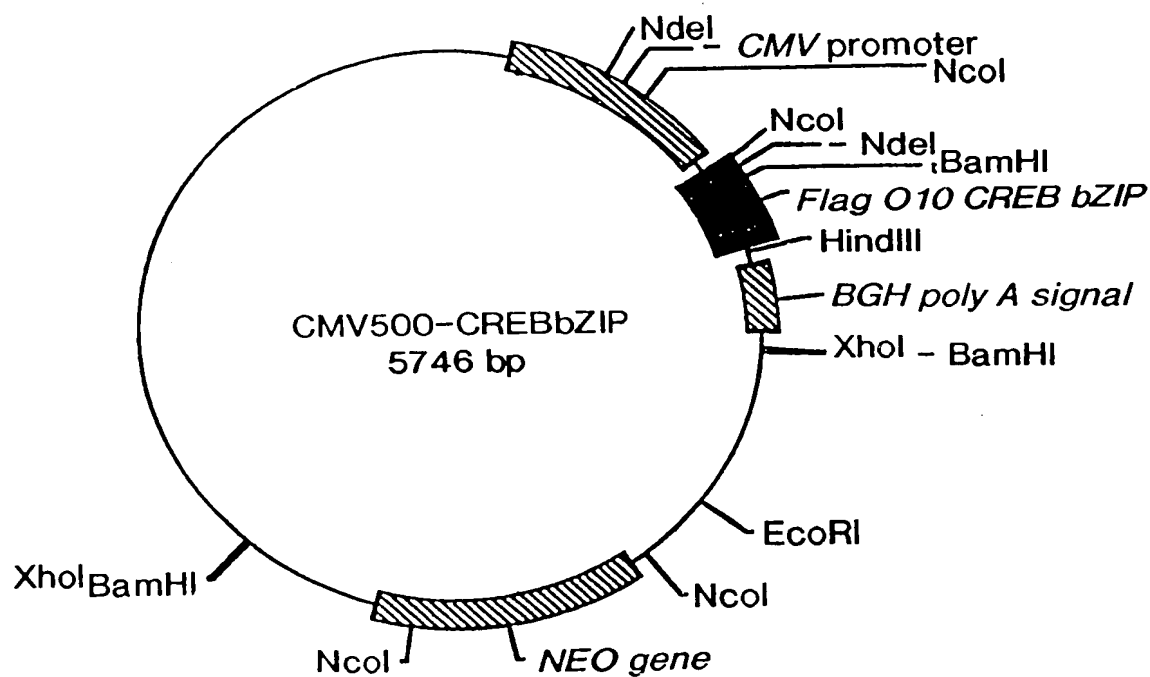
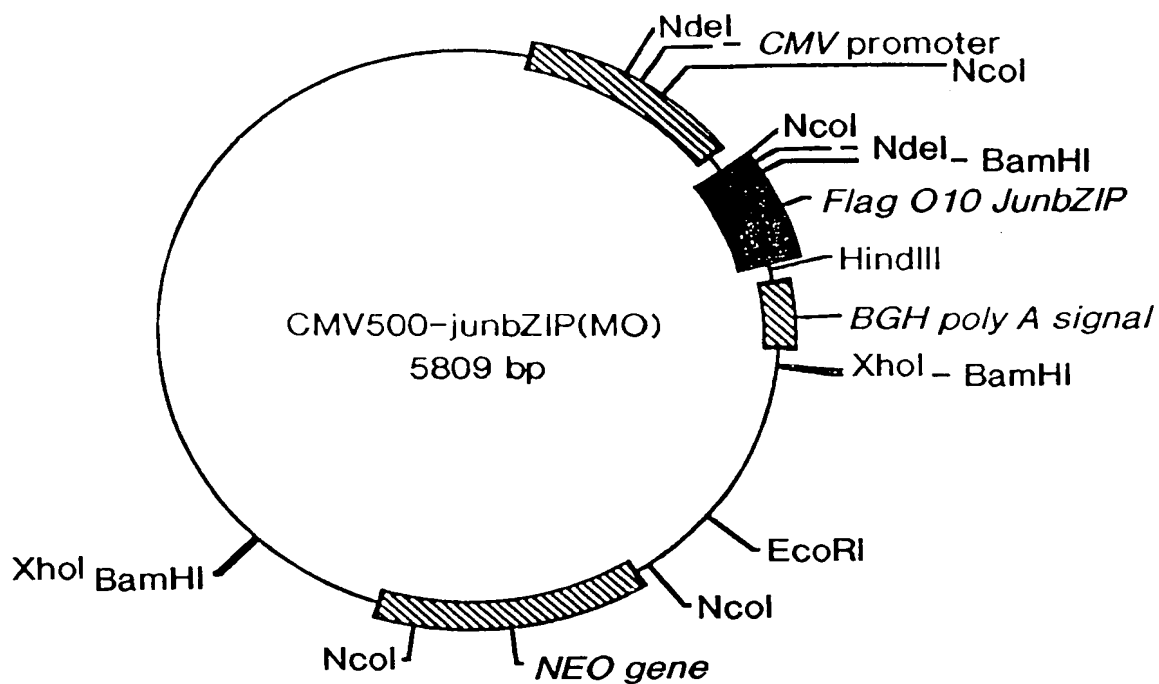


FIG. 16C

```

BamHI
10  *      *      *      *      *      *      *      *      *      *
GG ATCCC CTT CCT ACA CAG CCT GCT GAA GAA GCA CGA AAG AGA GAG GTT CGT
L  P  T  Q  P  A  E  E  A  A  R  K  R  E  V  R>
__a__CREB (AA 1-341);  NCBI GI: 56005; CODON_START=1; __a__>

60  *      *      *      *      *      *      *      *      *      *
CTA ATG AAG AAC AGG GAA GCA GCA AGA GAA TGT CGT AGA AAG AAG AAA
L  M  K  N  R  E  A  A  R  E  C  R  R  K  K  K>
__a__CREB (AA 1-341);  NCBI GI: 56005; CODON_START=1; __a__>

110 *      *      *      *      *      *      *      *      *      *
GAA TAT GTG AAA TGT TTA GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA
E  Y  V  K  C  L  E  N  R  V  A  V  L  E  N  Q>
__a__CREB (AA 1-341);  NCBI GI: 56005; CODON_START=1; __a__>

160 *      *      *      *      *      *      *      *      *      *
AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC
N  K  T  L  I  E  E  L  K  A  L  K  D  L  Y  C>
__a__CREB (AA 1-341);  NCBI GI: 56005; CODON_START=1; __a__>

200 *      *      *      *      *      *      *      *      *      *
CAC AAG TCA GAT TAA TTC AAG CTT
H  K  S  D  *>
__CREB (AA 1-3__>
HindIII

```

FIG. 17

[illegible]

★ Hind III

| | | | | | | | | | |
|----------------------------------------------------------------------|--|---------------------------------------|--|------------|--|----------|--|----------|--|
| 910 | | 920 | | 930 | | 940 | | D10 | |
| * NcoI | | * GAT | | * GAT | | * GAT | | * GAT | |
| CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT | | M D Y K D D D D K H M A S M T G> | | * NdeI | | * GAT | | * GAT | |
| 950 | | 960 | | 970 | | 980 | | 990 | |
| * GGA CAG CAA ATG GGT CGG GAT CCT GAC CTG GAA CAA CGT GCT GAG GAA | | * G Q Q M G R D P D L E Q R A E E> | | * BamHI | | * GAT | | * GAT | |
| 1000 | | 1010 | | 1020 | | 1030 | | 1040 | |
| * CTG GCC CGT GAA AAC GAA GAG CTG GAA AAA GAG GCC GAA GAG CTG GAG | | * L A R E N E E L E K E A E E L E> | | * GAT | | * GAT | | * GAT | |
| 1050 | | 1060 | | 1070 | | 1080 | | 1090 | |
| * CAG GAA CTG GCA GAA CTC GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA | | * Q E L A E L E N R V A V L E N Q> | | * GAT | | * GAT | | * GAT | |
| 1100 | | 1110 | | 1120 | | 1130 | | 1140 | |
| * AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC | | * N K T L I E E L K A L K D L Y C> | | * GAT | | * GAT | | * GAT | |
| 1150 | | 1160 | | 1170 | | 1180 | | 1190 | |
| * CAC AAG TCA GAT TAA TTC AAG CTT | | * H K S D * F [K L> | | * GAT | | * GAT | | * GAT | |

FIG. 19

Hind III

BamH I 10 20 30 40
 * * * * *
 GGATCCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAA GAG AAA AGG AGA
 P D K V E Q> L S P E E E E K R R>
 ____1783 TO ____> ____2470_2466 TO 2573 OF HUM FOS _0__b____>

50 60 70 80 90
 * * * * * *
 ATC CGA AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG
 I R R E R N K M A A A K C R N R>
 ____2500_b____b____251_2466 TO 2573 OF HUM FOS _30_b____b____2540b____>

100 110 120 130 140
 * * * * * *
 AGG AGG GAG CTG ACT GAT ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA
 R R E L T D T L Q A> E T D Q L E>
 ____b_2_2466 TO 2573 OF HUM FOS _570b____> 26_2688 TO 3329 OF H____>

150 160 170 180 190
 * * * * * *
 GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT GCC AAC CTG CTG AAG GAG
 D E K S A L Q T E I A N L L K E>
 ____2710_c____c____272_2688 TO 3329 OF HUM FOS _40_c____c____2750c____>

200 210 220 230 240
 * * * * * *
 AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC TGC AAG
 K E K L E F I L A A H R P A C K>
 ____c_2760__c____c____2688 TO 3329 OF HUM FOS _2790__c____c____2800__>

250 260
 * * *
 ATC CCT GAT TAATTCAAGC TT
 I P> Hind III
 ____c____>

FIG. 20

900 * NcoI Flag NdeI $\phi 10$
 CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG
 M D Y K D D D D K D K H M A S M T G G Q Q M>

960 * BamHI
 GGT CGG GAT CCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAG AAA AGG AGA ATC CGA
 G R D P K V E Q L S P E E E K R I R>

1020 Fos b zip
 *
 AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG AGG AGG GAG CTG ACT GAT
 R E R N K M A A A K C R N R R E L T D>

1080 *
 ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT
 T L Q A E T D Q L E D E K S A L Q T E I>

1140 *
 GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC
 A N L L K E K E K L E F I L A A H R P A>

1200 * HindIII
 TGC AAG ATC CCT GAT TAA GCCTT
 C K I P D *>

FIG. 21

FIG. 22

```

>NdeI
|
* 10      20      30      40      50
*  *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
M  A  S  M  T  G  G  Q  Q  M  G  R>
__a__a__a__a__a__a_F10__a__a__a__a__a__a__>
                                     D  P>
                                     __b__>

        60      70      80      90
        *      *      *      *      *
GAC CTG GAA CAA CGT GCT GAG GAA CTG GCC CGT GAA AAC GAA GAG CTG
D  L  E  Q  R  A  E  E  L  A  R  E  N  E  E  L>
__b__b__b__b__4HEPTAD ACIDIC EXTENSION__b__b__b__b__>

                                     >XhoI
                                     |
100      110      120      130      140
*      *      *      *      *      *
GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC GAG GCG
E  K  E  A  E  E  L  E  Q  E  N  A  E  L  E>
__b__b__b__b__4HEPTAD ACIDIC EXTENSION__b__b__b__b__>
                                     A>
                                     __>

        150      160      170      180      190
        *      *      *      *      *
GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT
E  T  D  Q  L  E  D  E  K  S  A  L  Q  T  E  I>
__c__c__c__c__c__c_C-FOS PROTEIN__c__c__c__c__c__c__>

        200      210      220      230      240
        *      *      *      *      *
GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT
A  N  L  L  K  E  K  E  K  L  E  F  I  L  A  A>
__c__c__c__c__c__c_C-FOS PROTEIN__c__c__c__c__c__c__>

                                     >HindIII
                                     |
        250      260      270      280
        *      *      *      *
CAC CGA CCT GCC TGC AAG ATC CCT GATT AATTC AAGCT T
H  R  P  A  C  K  I  P>
__c__C-FOS PROTEIN__c__c__>

```

| | | | | | | | | | | | | | | | | |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 900 | | | | | | | | | | | | | | | | |
| * NcoI | | | | | | | | | | | | | | | | |
| CC | ATG | GAC | TAC | AAG | GAC | GAC | GAT | GAC | AAG | CAT | ATG | GCT | AGC | ATG | ACT | GGT |
| | M | D | Y | K | D | D | D | D | K | H | M | A | S | M | T | G> |
| | M | D | Y | K | D | D | D | D | K | H | M | A | S | M | T | G> |
| <div> <div>Flag</div> <div>960</div> <div>BamHI</div> <div>Ø10</div> </div> | | | | | | | | | | | | | | | | |
| GGA | CAG | CAA | ATG | GGT | CGG | GAT | CCT | GAC | CTG | GAA | CAA | CGT | GCT | GAG | GAA | |
| G | Q | Q | M | G | R | D | P | D | L | E | Q | R | A | E | E> | |
| G | Q | Q | M | G | R | D | P | D | L | E | Q | R | A | E | E> | |
| 1020 | | | | | | | | | | | | | | | | |
| * | | | | | | | | | | | | | | | | |
| CTG | GCC | CGT | GAA | AAC | GAA | GAG | CTG | GAA | AAA | GAG | GCC | GAA | GAG | CTG | GAG | |
| L | A | R | E | N | E | E | L | E | K | E | A | E | E | L | E> | |
| L | A | R | E | N | E | E | L | E | K | E | A | E | E | L | E> | |
| 1080 | | | | | | | | | | | | | | | | |
| * | | | | | | | | | | | | | | | | |
| CAG | GAA | AAC | GCT | GAA | CTC | GAG | GCG | GAG | ACA | GAC | CAA | CTA | GAA | GAT | GAG | |
| Q | E | N | A | E | L | E | A | E | T | D | Q | L | E | D | E> | |
| Q | E | N | A | E | L | E | A | E | T | D | Q | L | E | D | E> | |
| <div> <div>AAG</div> <div>TCT</div> <div>GCT</div> <div>TTG</div> <div>CAG</div> <div>ACC</div> <div>GAG</div> <div>ATT</div> <div>GCC</div> <div>AAC</div> <div>CTG</div> <div>CTG</div> <div>AAG</div> <div>GAG</div> <div>AAG</div> <div>GAA</div> </div> | | | | | | | | | | | | | | | | |
| K | S | A | L | Q | T | E | I | A | N | L | L | K | E | K | E> | |
| K | S | A | L | Q | T | E | I | A | N | L | L | K | E | K | E> | |
| 1140 | | | | | | | | | | | | | | | | |
| * | | | | | | | | | | | | | | | | |
| AAA | CTA | GAG | TTC | ATC | CTG | GCA | CCT | CAC | CGA | CCT | GCC | TGC | AAG | ATC | CCT | |
| K | L | E | F | I | L | A | A | H | R | P | A | C | K | I | P> | |
| K | L | E | F | I | L | A | A | H | R | P | A | C | K | I | P> | |
| <div> <div>GAT</div> <div>TAA</div> <div>GCTT</div> <div>Hind III</div> </div> | | | | | | | | | | | | | | | | |
| D | * | > | | | | | | | | | | | | | | |
| D | * | > | | | | | | | | | | | | | | |

FIG. 23

900 * NcoI Flag NdeI Ø10
 CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG
 M D Y K D D D D K H M A S M T G G Q Q M>

960 * BamHI
 GGT CCG GAT CCC TCC CCT ATT GAC ATG GAG TCG CAG GAG AGA ATC AAA GCC GAG AGA AAA
 G R D P S P I D M E S Q E R I K A E R K>

1020 Jun b zip
 * CGC ATG AGA AAC AGA ATT GCG GCG TCC AAA TGC CGG AAA AGG AAG TTG GAA AGG ATT GCC
 R M R N R I A A S K C R K R K L E R I A>

1080 *
 AGG TTG GAA GAA AAA GTG AAA ACT TTG AAA GCC CAG AAC TCA GAG CTG GCA TCC ACG GCC
 R L E E K V K T L K A Q N S E L A S T A>

1140 *
 AAC ATG CTC AGA GAA CAG GTT GCA CAG CTT AAG CAG AAG GTC ATG AAC CAT GTC AAC AGC
 N M L R E Q V A Q L K Q K V M N H V N S>

1200 * HdIII
 GGG TGC CAG CTA ATG CTA ACA CAA CAG TTG CAA ACG TTT TGA TTC AAGCTT
 G C Q L M L T Q Q Q L Q T F * F>

FIG. 24

FIG. 25

```

>NdeI
|
4090      4100      4110      4120      4130
* | *      *      *      *      *
ATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCC GAC
  M   A   S   M   T   G   G   Q   Q   M   G   R>
  _a_ _a_ _a_ _a_ _a_ F10 _a_ _a_ _a_ _a_ _a_>
                                     D   P   D>
                                     _b_ _b_>

>XhoI
|
4140      4150      4160      4170      4180
* | *      *      *      *      *
GAA GAG GAA GAT GAC GAA GAA GAA CTC GAG GAA CTG GAA GAC AGC TTT
  E   E   E   D   D   E   E   E   L   E   E   L   E>
  _b_ _b_ _b_ _b_ _b_ POLY-GLU _b_ _b_ _b_ _b_ _b_>
                                     D   S   F>
                                     _c_ _c_>

4190      4200      4210      4220      4230
* | *      *      *      *      *
CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC CAA GGA GAG AAG GCA TCC
  H   S   L   R   D   S   V   P   S   L   Q   G   E   K   A   S>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_>

4240      4250      4260      4270
* | *      *      *      *      *
CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG TAT ATC CAG TAT ATG CGA
  R   A   Q   I   L   D   K   A   T   E   Y   I   Q   Y   M   R>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_>

4280      4290      4300      4310      4320
* | *      *      *      *      *
AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT GAT GAC CTC AAG CGG CAG
  R   K   N   H   T   H   Q   Q   D   I   D   D   L   K   R   Q>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_>

4330      4340      4350      4360      4370
* | *      *      *      *      *
AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA CTG GAG AAG GCA AGA TCA
  N   A   L   L   E   Q   Q   V   R   A   L   E   K   A   R   S>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_>

>HindIII
|
4380      4390      4400
* | *      *      *
AGT GCC CAA CTG CAG ACC TGAGGCAA GCTTATC
  S   A   Q   L   Q   T>
  _MAX BHLH DOMAIN _c_>

```

FIG. 26

```

>NdeI
|
4090          4100          4110          4120          4130
* | *          *          *          *          *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
      M  A  S  M  T  G  G  Q  Q  M  G  R>
      _a_a_a_a_a_a_F10_a_a_a_a_a_a_>
                                     D  P>
                                     _b_>

                                     >XhoI
                                     |
4140          4150          4160          4170
* | *          *          *          *          *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D  L  E  K  E  A  E  E  L  E  Q  E  N  A  E  L>
_b_b_TWO AMPHIPATHIC HEPTAD S (1st PHASE- 783) _b_b_>

4180          4190          4200          4210          4220
* | *          *          *          *          *
GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC
E  L  E>
_b_b_>
      D  S  F  H  S  L  R  D  S  V  P  S  L>
      _c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

4230          4240          4250          4260          4270
* | *          *          *          *          *
CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG
Q  G  E  K  A  S  R  A  Q  I  L  D  K  A  T  E>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280          4290          4300          4310          4320
* | *          *          *          *          *
TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT
Y  I  Q  Y  M  R  R  K  N  H  T  H  Q  Q  D  I>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330          4340          4350          4360          4370
* | *          *          *          *          *
GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA
D  D  L  K  R  Q  N  A  L  L  E  Q  Q  V  R  A>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

                                     >HindIII
                                     |
4380          4390          4400          4410          4420
* | *          *          *          *          *
CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGA GGCAAGCTTA
L  E  K  A  R  S  S  A  Q  L  Q  T>
_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

```

FIG. 27

```

>NdeI
|
4090          4100          4110          4120          | 4130
* | *      *      *      *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
      M  A  S  M  T  G  G  Q  Q  M  G  R>
      _a_a_a_a_a_a_F10_a_a_a_a_a_a_>
                                          D  P>
                                          _b_>

                                          >XhoI
                                          |
4140          4150          4160          4170
* | *      *      *      *      *      *      *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
      D  L  E  K  E  A  E  E  L  E  Q  E  N  A  E  L>
      _b_b_TWO AMPHIPATHIC HEPTAD S (2ND PHASE- 784)_b_b_>

4180          4190          4200          4210          4220
* | *      *      *      *      *      *      *
GAG GAA CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA
      E  E  L  E>
      _TWO AMPH_>
      D  S  F  H  S  L  R  D  S  V  P  S>
      _c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

4230          4240          4250          4260          4270
* | *      *      *      *      *      *      *
CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA
      L  Q  G  E  K  A  S  R  A  Q  I  L  D  K  A  T>
      _c_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_c_>

4280          4290          4300          4310          4320
* | *      *      *      *      *      *      *
GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC
      E  Y  I  Q  Y  M  R  R  K  N  H  T  H  Q  Q  D>
      _c_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_c_>

4330          4340          4350          4360          4370
* | *      *      *      *      *      *      *
ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT
      I  D  D  L  K  R  Q  N  A  L  L  E  Q  Q  V  R>
      _c_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_c_>

                                          >HindIII
                                          |
4380          4390          4400          4410          4420
* | *      *      *      *      *      *      *
GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCAAGC
      A  L  E  K  A  R  S  S  A  Q  L  Q  T>
      _c_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_c_>

```

TTATC

FIG. 28

```

>NdeI
|
4090          4100          4110          4120          4130
* | *      *      *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
M   A   S   M   T   G   G   Q   Q   M   G   R>
__a__a__a__a__a__a_F10__a__a__a__a__a__a__>
                                     D   P>
                                     __b__>

                                     >XhoI
                                     |
4140          4150          4160          4170
* | *      *      *      *      *      *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D   L   E   K   E   A   E   E   L   E   Q   E   N   A   E   L>
__b__b__TWO AMPHIPATHIC HEPTAD S (3D PHASE- 785) __b__b__>

4180          4190          4200          4210          4220
* | *      *      *      *      *      *
GAG GAA GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA
E   E   E   L   E>
__TWO AMPHIPAT__>
                                     D   S   F   H   S   L   R   D   S   V   P>
                                     __c__c__c__MAX BHLH DOMAIN__c__c__c__>

4230          4240          4250          4260          4270
* | *      *      *      *      *      *
TCA CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA
S   L   Q   G   E   K   A   S   R   A   Q   I   L   D   K   A>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

4280          4290          4300          4310          4320
* | *      *      *      *      *      *
ACA GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA
T   E   Y   I   Q   Y   M   R   R   K   N   H   T   H   Q   Q>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

4330          4340          4350          4360          4370
* | *      *      *      *      *      *
GAC ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC
D   I   D   D   L   K   R   Q   N   A   L   L   E   Q   Q   V>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

                                     >HindIII
                                     |
4380          4390          4400          4410          4420
* | *      *      *      *      *      *
CGT GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCA
R   A   L   E   K   A   R   S   S   A   Q   L   Q   T>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

*
AGCTTATC

```


BamHI 10 20 30 40
 * * * * * *
GGATCCC AAC GAC AAG AGG CGG ACA CAC AAC GTC TTG GAA CGT CAG AGG
 N D K R R T H N V L E R Q R>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC ___>

50 60 70 80 90
 * * * * * *
 AGG AAC GAG CTG AAG CGC AGC TTT TTT GCC CTG CGT GAC CAG ATC CCT
 R N E L K R S F F A L R D Q I P>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

100 110 120 130 140
 * * * * * *
 GAA TTG GAA AAC AAC GAA AAG GCC CCC AAG GTA GTG ATC CTC AAA AAA
 E L E N N E K A P K V V I L K K>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

150 160 170 180 190
 * * * * * *
 GCC ACC GCC TAC ATC CTG TCC ATT CAA GCA GAC GAG CAC AAG CTC ACC
 A T A Y I L S I Q A D E H K L T>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

200 210 220 230 240
 * * * * * *
 TCT GAA AAG GAC TTA TTG AGG AAA CGA CGA GAA CAG TTG AAA CAC AAA
 S E K D L L R K R R E Q L K H K>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

250 260 270
 * * * * *
 CTC GAA CAG CTT CGA AAC TCT GGT GCA TAA AAGCTT
 L E Q L R N S G A *> Hind III
 ___PUTATIVE; NCBI GI: 50468; CODON___>

FIG. 29

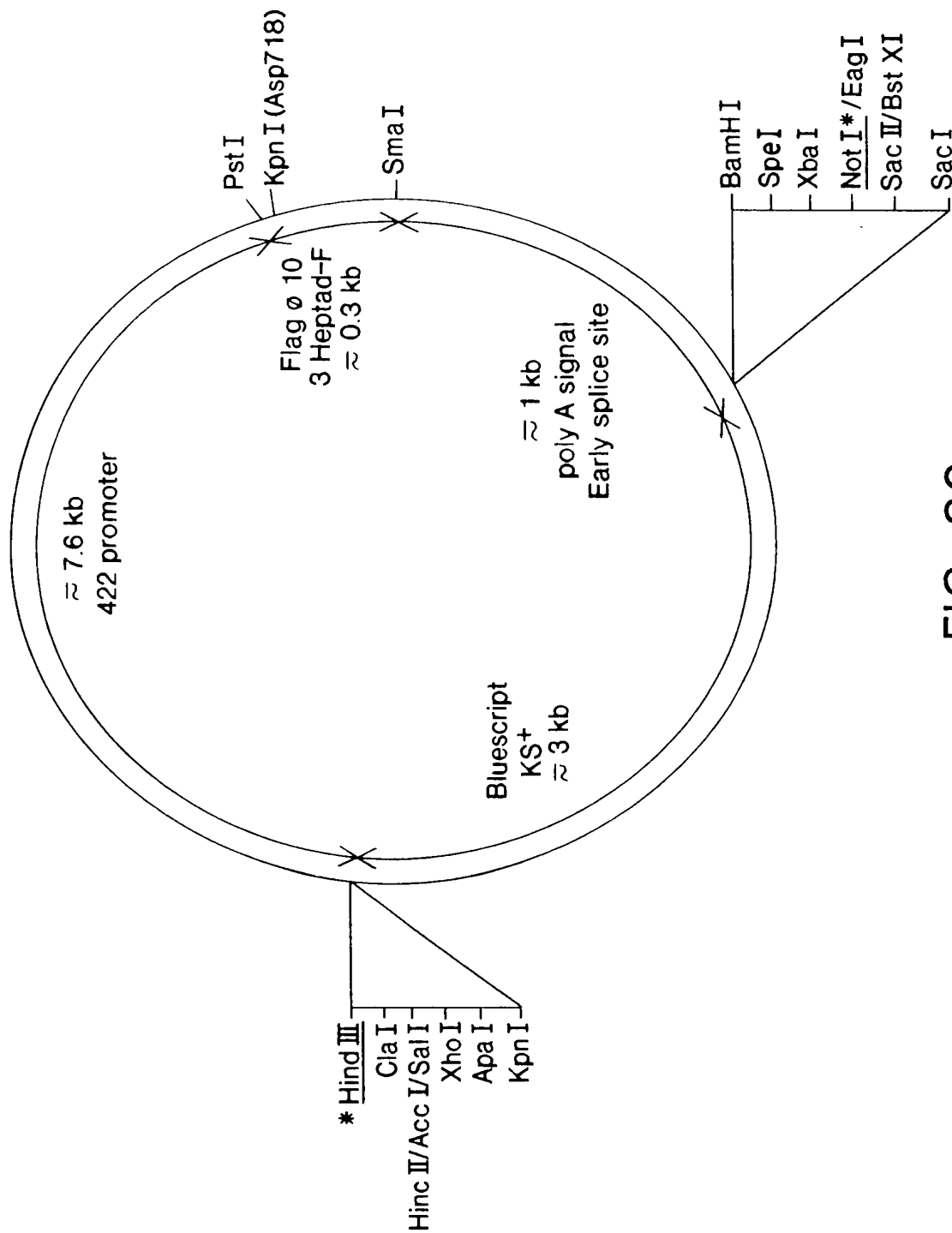


FIG. 30

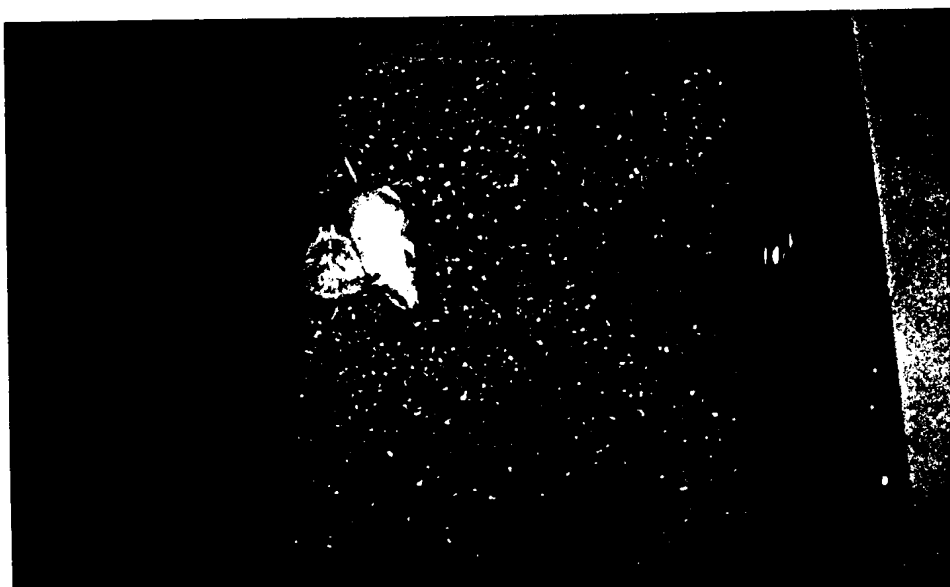


FIG. 31